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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/987,701

DATE: 12/06/2001
TIME: 15:06:11

Input Set : A:\es.txt
Output Set: N:\CRF3\12062001\I987701.raw

ENTERED

3 <110> APPLICANT: BASCH, Ross S.
 4 ZHANG, Xin-Min
 6 <120> TITLE OF INVENTION: PROTEIN THAT MODULATES THE STABILITY OF TRANSCRIPTIONAL
 REGULATORY
 7 COMPLEXES REGULATING NUCLEAR HORMONE RECEPTOR ACTIVITY, DNA ENCODING SAME, AND
 8 ANTIBODIES THERETO
 10 <130> FILE REFERENCE: BASCH=1A
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/987,701
 13 <141> CURRENT FILING DATE: 2001-11-15
 15 <150> PRIOR APPLICATION NUMBER: 60/248,191
 16 <151> PRIOR FILING DATE: 2000-11-15
 18 <160> NUMBER OF SEQ ID NOS: 17
 20 <170> SOFTWARE: PatentIn version 3.1
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 3885
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Homo sapiens
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 29 <222> LOCATION: (161)..(1705)
 30 <223> OTHER INFORMATION:
 33 <220> FEATURE:
 34 <221> NAME/KEY: misc_feature /
 35 <222> LOCATION: (2487)..(2487)
 36 <223> OTHER INFORMATION: n is a, c, g or t.
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 50 tatccctgtgt tgtgacctca tggttaagt gggataaaag atg agt ata agc agt 175
 51 Met Ser Ile Ser Ser
 52 1 5
 54 gat gag gtc aac ttc ttg gta tat aga tac ttg caa gag tca gga ttt 223
 55 Asp Glu Val Asn Phe Leu Val Tyr Arg Tyr Leu Gln Glu Ser Gly Phe
 56 10 15 20
 58 tct cat tca gca ttt acc ttt ggt ata aaa agc cat atc agt cag tcc 271
 59 Ser His Ser Ala Phe Thr Phe Gly Ile Lys Ser His Ile Ser Gln Ser
 60 25 30 35
 62 aat ata aat ggt gcc ctc gtc cca ccc gct gca ttg att tct atc atc 319
 63 Asn Ile Asn Gly Ala Leu Val Pro Pro Ala Ala Leu Ile Ser Ile Ile
 64 40 45 50
 66 cag aaa ggt cta cag tat gta gaa gca gaa gtt agt att aat gag gat 367
 67 Gln Lys Gly Leu Gln Tyr Val Glu Ala Glu Val Ser Ile Asn Glu Asp
 68 55 60 65
 70 ggt acc ttg ttt gat ggt cga cca ata gag tct ctg tcc ctg ata gat 415

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71	Gly	Thr	Leu	Phe	Asp	Gly	Arg	Pro	Ile	Glu	Ser	Leu	Ser	Leu	Ile	Asp		
72	70					75				80						85		
74	gcc	gta	atg	cct	gat	gta	caa	aca	aga	caa	caa	gct	tat	aga	gat		463	
75	Ala	Val	Met	Pro	Asp	Val	Val	Gln	Thr	Arg	Gln	Gln	Ala	Tyr	Arg	Asp		
76						90				95						100		
78	aag	ctt	gca	cag	caa	cag	gca	gca	gct	gct	gca	gct	gca	gct	gca		511	
79	Lys	Leu	Ala	Gln	Gln	Gln	Ala											
80						105				110						115		
82	gcc	agc	caa	caa	gga	tct	gca	aaa	aat	gga	gaa	aac	aca	gca	aat	ggg		559
83	Ala	Ser	Gln	Gln	Gly	Ser	Ala	Lys	Asn	Gly	Glu	Asn	Thr	Ala	Asn	Gly		
84						120				125						130		
86	gag	gag	aat	gga	gca	cat	act	ata	gca	aat	aat	cat	act	gat	atg	atg		607
87	Glu	Glu	Asn	Gly	Ala	His	Thr	Ile	Ala	Asn	Asn	His	Thr	Asp	Met	Met		
88						135				140						145		
90	gaa	gtg	gat	ggg	gat	gtt	gaa	atc	cct	aat	aaa	gct	gtt	gtg	ttg		655	
91	Glu	Val	Asp	Gly	Asp	Val	Glu	Ile	Pro	Pro	Asn	Lys	Ala	Val	Val	Leu		
92						150				155						160	165	
94	cgg	ggc	cat	gaa	tct	gaa	gtt	ttt	atc	tgt	gcc	tgg	aac	cct	gtt	agt		703
95	Arg	Gly	His	Glu	Ser	Glu	Val	Phe	Ile	Cys	Ala	Trp	Asn	Pro	Val	Ser		
96						170				175						180		
98	gat	ctc	cta	gca	tca	ggg	tct	gga	gac	tca	aca	gca	aga	ata	tgg	aat		751
99	Asp	Leu	Leu	Ala	Ser	Gly	Ser	Gly	Asp	Ser	Thr	Ala	Arg	Ile	Trp	Asn		
100						185				190						195		
102	ctt	agt	gag	aac	agc	acc	agt	ggc	tct	aca	cag	tta	gta	ctt	aga	cat		799
103	Leu	Ser	Glu	Asn	Ser	Thr	Ser	Gly	Ser	Thr	Gln	Leu	Val	Leu	Arg	His		
104						200				205						210		
106	tgt	ata	cga	gaa	gga	ggg	caa	gat	gtt	ccg	agc	aac	aag	gat	gtc	aca		847
107	Cys	Ile	Arg	Glu	Gly	Gly	Gln	Asp	Val	Pro	Ser	Asn	Lys	Asp	Val	Thr		
108						215				220						225		
110	tct	cta	gat	tgg	aat	agt	gaa	ggt	aca	ctt	cta	gca	act	ggt	tcc	tat		895
111	Ser	Leu	Asp	Trp	Asn	Ser	Glu	Gly	Thr	Leu	Leu	Ala	Thr	Gly	Ser	Tyr		
112						230				235						240	245	
114	gat	ggg	ttt	gcc	aga	ata	tgg	act	aaa	gat	ggt	aac	ctt	gct	agc	acc		943
115	Asp	Gly	Phe	Ala	Arg	Ile	Trp	Thr	Lys	Asp	Gly	Asn	Leu	Ala	Ser	Thr		
116						250				255						260		
118	tta	ggg	cag	cat	aaa	ggc	cct	ata	ttt	gca	tta	aaa	tgg	aat	aag	aaa		991
119	Leu	Gly	Gln	His	Lys	Gly	Pro	Ile	Phe	Ala	Leu	Lys	Trp	Asn	Lys	Lys		
120						265				270						275		
122	gga	aat	ttc	atc	cta	agt	gct	gga	gta	gac	aag	act	aca	att	att	tgg		1039
123	Gly	Asn	Phe	Ile	Leu	Ser	Ala	Gly	Val	Asp	Lys	Thr	Thr	Ile	Ile	Trp		
124						280				285						290		
126	gac	gca	cat	act	ggt	gaa	gcc	aag	caa	cag	ttt	cct	ttt	cat	tca	gca		1087
127	Asp	Ala	His	Thr	Gly	Glu	Ala	Lys	Gln	Gln	Phe	Pro	Phe	His	Ser	Ala		
128						295				300						305		
130	cca	gca	ttg	gat	ttt	gat	tgg	cag	agc	aac	acc	ttt	gct	tct	tgt		1135	
131	Pro	Ala	Leu	Asp	Val	Asp	Trp	Gln	Ser	Asn	Asn	Thr	Phe	Ala	Ser	Cys		
132						310				315						320	325	
134	agt	aca	gat	atg	tgc	att	cat	gtc	tgt	aaa	tta	gga	caa	gac	aga	cct		1183
135	Ser	Thr	Asp	Met	Cys	Ile	His	Val	Cys	Lys	Leu	Gly	Gln	Asp	Arg	Pro		

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138 att aaa aca ttc caa gga cat acg aat gaa gta aat gct atc aaa tgg				1231
139 Ile Lys Thr Phe Gln Gly His Thr Asn Glu Val Asn Ala Ile Lys Trp				
140 345	350	355		
142 gac cca act ggc aat ctc ttg gcc tcc tgt tct gac gac atg act tta				1279
143 Asp Pro Thr Gly Asn Leu Leu Ala Ser Cys Ser Asp Asp Met Thr Leu				
144 360	365	370		
146 aag ata tgg agt atg aaa caa gac aat tgt gtc cat gat ttg cag caa				1327
147 Lys Ile Trp Ser Met Lys Gln Asp Asn Cys Val His Asp Leu Gln Gln				
148 375	380	385		
150 cat aat aaa gaa att tat act atc aaa tgg agt cca aca gga cca ggg				1375
151 His Asn Lys Glu Ile Tyr Thr Ile Lys Trp Ser Pro Thr Gly Pro Gly				
152 390	395	400	405	
154 act aat aat cca aat gcc aac ctt atg tta gca agt gca tcc ttt gat				1423
155 Thr Asn Asn Pro Asn Ala Asn Leu Met Leu Ala Ser Ala Ser Phe Asp				
156 410	415	420		
158 tct act gtt agg tta tgg gat gta gac cga ggg ata tgc atc cat acc				1471
159 Ser Thr Val Arg Leu Trp Asp Val Asp Arg Gly Ile Cys Ile His Thr				
160 425	430	435		
162 ttg aca aaa cac caa gag cct gtg tac agt gta gct ttc agt cct gat				1519
163 Leu Thr Lys His Gln Glu Pro Val Tyr Ser Val Ala Phe Ser Pro Asp				
164 440	445	450		
166 ggc agg tat ctg gca agt ggt tct ttt gac aaa tgt gta cac atc tgg				1567
167 Gly Arg Tyr Leu Ala Ser Gly Ser Phe Asp Lys Cys Val His Ile Trp				
168 455	460	465		
170 aac acg cag aca ggt gct cta gtt cac agc tat agg gga aca ggt gga				1615
171 Asn Thr Gln Thr Gly Ala Leu Val His Ser Tyr Arg Gly Thr Gly Gly				
172 470	475	480	485	
174 ata ttt gaa gtt tgc tgg aat gca gca gga gac aaa gtt gga gcc agt				1663
175 Ile Phe Glu Val Cys Trp Asn Ala Ala Gly Asp Lys Val Gly Ala Ser				
176 490	495	500		
178 gca tca gat ggt tca gtt tgt gta tta gac ctt cg ^a aaa tag				1705
179 Ala Ser Asp Gly Ser Val Cys Val Leu Asp Leu Arg Lys				
180 505	510			
182 cgctactagt tggaaaggcat ggaccgacta tgaatgtgta catagccaaa atgagtgtcc				1765
184 ctgaccatg taatgttata gtcccacttg aaccatggcc agtccaatac agccaaatct				1825
186 aaaagaataa tatacataca gtgtatataa acaaaaattac accctgaaga tgacagagtt				1885
188 ttgtcacagc ttgtgaattc ttgtcaccaa gtgctgaaat ctaatctgct gtgccctaa				1945
190 aatagcattt agaagtttg gatatgaaaa acagaagaga gaaaatatac attataaaag				2005
192 cagtacatac atgtaccagt tttggatatac taaatgacag cttgtttct ccccttgaa				2065
194 tcagcagaca ccatggatta tattctttt ttcccttcag tagtgacag tttgtatgta				2125
196 cagagaaaaat ggacttacaa aaacttgcag cagtagttt ttcttgctt aaaaatttcgt				2185
198 ttttggttta gattatggat gcatgaagta agggagtgaa tcagtttctt gtttatattt				2245
200 ttttcacctt ttaaacaaaa aattctttaa aatattttaa tgcattctt tgaagaggt				2305
202 gatgttttgtt acattttatg gctcccagag catatattca gttggtgcat gttgtggaa				2365
204 gggaaattgg aaattaaatg gaaaacatcat gacttggtc ctgtcaatct gtaagacaca				2425
206 tcagtaaaaaa ggtattatgc tctgttggtt ttgtttttt gttttgtttt tttttttttt				2485
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210 tctgccaattt aaagactaga agggcacaac tttttttta attaccatag agaagataca				2605

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212 taaaaaaaaa tcttctgatg ttttagcc ataactaaat tatggtaaaa atgtgcacta 2665
 214 ttgtaaaaag gagcaacgta gtttgggtt ttttgtt ttttgtttt gctttttt 2725
 216 ttaagagatt aaaatgttc tgataagga ttagctc gaagtgtcca tcattctgt 2785
 218 tanaagctta aatatgtaat gtaaccaaac tccagttata aaaatctctc atgttgg 2845
 220 ctttatacaa agcaagataa cgcatataa cactgcatt acatggcaaa atgttgcta 2905
 222 ccttagttt aaaaacaatc tcaaacaaaa gacttgcctc aagggtttt taaatagcag 2965
 224 tgatccagaa ttttttttta tgaaagtata attgcactaa ccttcttcct gctgctctga 3025
 226 ttctgcattt gtggacttg tgactacgtt tttcaata tagatagatt taagctgcta 3085
 228 atttttttt ttttagtaat cactactata tcattgtctt tactctgttt ataataatcaa 3145
 230 gtattttctt aaagatatag atattaaacc ttgtgctcat gcaacttaga gtaacatata 3205
 232 cagacaaatg attgcattttt gcatgttta tatgtgtgac taataaggct tgcatttttt 3265
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 240 tttaacccaa gtaatgcacg tttgattgtt ttcagcattt gtgttgc tatttttaca 3505
 242 aaacagcatt gattgaagca agttttgggtt ttactaaggt aggttagcat ttgttattgg 3565
 244 taaagagaat aaatacacact aatttcacaa tacattgtta tatgttacccc agttttgtt 3625
 246 agtggggact atgatactgt aataatattt ttaaaaattt acatcaagag aggcaactcat 3685
 248 tcacatgggt tttgtgccag ctcttttag gggtttggat cacatttagag atatttagaa 3745
 250 catattaccc tgtgacttac gtagggaaacc taatatgctg agtatctggc acttgaattc 3805
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 273 His Ile Ser Gln Ser Asn Ile Asn Gly Ala Leu Val Pro Pro Ala Ala
 274 35 40 45
 277 Leu Ile Ser Ile Ile Gln Lys Gly Leu Gln Tyr Val Glu Ala Glu Val
 278 50 55 60
 281 Ser Ile Asn Glu Asp Gly Thr Leu Phe Asp Gly Arg Pro Ile Glu Ser
 282 65 70 75 80
 285 Leu Ser Leu Ile Asp Ala Val Met Pro Asp Val Val Gln Thr Arg Gln
 286 85 90 95
 289 Gln Ala Tyr Arg Asp Lys Leu Ala Gln Gln Gln Ala Ala Ala Ala
 290 100 105 110
 293 Ala Ala Ala Ala Ala Ser Gln Gln Gly Ser Ala Lys Asn Gly Glu
 294 115 120 125
 297 Asn Thr Ala Asn Gly Glu Glu Asn Gly Ala His Thr Ile Ala Asn Asn
 298 130 135 140
 301 His Thr Asp Met Met Glu Val Asp Gly Asp Val Glu Ile Pro Pro Asn
 302 145 150 155 160
 305 Lys Ala Val Val Leu Arg Gly His Glu Ser Glu Val Phe Ile Cys Ala

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314	195	200	205
317	Leu Val Leu Arg His Cys Ile Arg Glu Gly Gly Gln Asp Val Pro Ser		
318	210	215	220
321	Asn Lys Asp Val Thr Ser Leu Asp Trp Asn Ser Glu Gly Thr Leu Leu		
322	225	230	235
325	240	245	250
326	Ala Thr Gly Ser Tyr Asp Gly Phe Ala Arg Ile Trp Thr Lys Asp Gly		
329	255	260	265
330	Asn Leu Ala Ser Thr Leu Gly Gln His Lys Gly Pro Ile Phe Ala Leu		
333	270	275	280
334	285	290	295
337	Thr Thr Ile Ile Trp Asp Ala His Thr Gly Glu Ala Lys Gln Gln Phe		
338	300	305	310
341	320	325	330
342	Pro Phe His Ser Ala Pro Ala Leu Asp Val Asp Trp Gln Ser Asn Asn		
345	335	340	345
346	350	355	360
349	365	370	375
353	Gly Gln Asp Arg Pro Ile Lys Thr Phe Gln Gly His Thr Asn Glu Val		
354	380	385	390
357	395	395	400
358	400	405	410
361	415	420	425
362	430	435	440
365	445	450	455
366	460	465	470
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VERIFICATION SUMMARY
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Input Set : A:\es.txt
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L:208 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:218 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:263 M:283 W: Missing Blank Line separator, <400> field identifier